

GenCore version 6.2  
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OM nucleic - nucleic search, using sw model

Run on: January 29, 2007, 11:54:23 ; Search time 1 Seconds  
(without alignments)

**Title:** US-10-780-507-24-COPY  
**Perfect score:** 1503

Sequence: 1 atgggtgcgagagcgtcagt.....acgacccctcgtcacaataa 1503

Scoring table: IDENTITY NUC.

Gapop 10.0<sup>-</sup>, Gapext 0.5

Searched: 1 seqs, 1532 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match 100\$  
Listing first 45 summaries

Database : US09017981.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	899.8	59.9	1532	1	US-09-017-981-1
2	18.2	1.2	1532	1	US-09-017-981-1

## ATTACHMENTS

```

RESULT 1
US-09-017-981-1
; Sequence 1, Application US/09017981
; GENERAL INFORMATION:
;   APPLICANT: Shiver, John W.
;   APPLICANT: Davies, Mary Ellen
;   APPLICANT: Freed, Daniel C.
;   APPLICANT: Liu, Margaret A.
;   APPLICANT: Perry, Helen C.
; TITLE OF INVENTION: Synthetic HIV Gag Genes
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Merck & Co., Inc.
;   STREET: P.O. Box 2000, 126 E. Lincoln Ave.
;   CITY: Rahway
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 07065-0900
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows
; SOFTWARE: FastSQL for Windows Version 2.0.b
; CURRENT APPLICATION NUMBER: US/09/017,981
; FILING DATE: 03-FEB-1998

```



Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 sn

Database : US09017981.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	920.6	61.3	1532	1	US-09-017-981-1	Sequence 1, Appli
2	19.6	1.3	1532	1	US-09-017-981-1	Sequence 1, Appli
C						

## ALIGNMENTS

## RESULT 1

```

US-09-017-981-1
; Sequence 1, Application US/09017981
; GENERAL INFORMATION:
; APPLICANT: Shiver, John W.
; APPLICANT: Davies, Mary Ellen
; APPLICANT: Freed, Daniel C.
; APPLICANT: Liu, Margaret A.
; APPLICANT: Perry, Helen C.
; TITLE OP INVENTION: Synthetic HIV Gag Genes
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA

```

```

COMPAR: 038
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSQL for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017.98

```

APPLICATION NUMBER: 03/03/017,381  
FILING DATE: 03-FEB-1998

CLASSIFICATION: 536

; P R I O R A P P L I C A T I O N D A T A :

APPLICATION NUMBER: US60/037,854

FILING DATE: 07-FEB-1997

APPLICATION NUMBER: GB9705040.5

FILING DATE: 12-MAR-1997

ATTORNEY/AGENT INFORMATION:  
NAME: HAND J Mark

NAME: HALL, C. MARK  
REGISTRATION NUMBER: 36-545

REFERENCE/DOCKET NUMBER: 19730

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-3905

**TELEFAX: 732-594-4720**

TELEX:

; INFORMATION FOR SEQ ID NO: 1:  
; DEFINING CHARACTERISTICS:; SEQUENCE CHARACTERISTICS:  
LENGTH. 1522 base pairs

LENGTH: 1552 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both

MOLECULE TYPE: cdna

;  
;  
; **HYPOTHETICAL: NO**

; ANTI-SENSE: NO

US-09-017-981-1

Query Match 61.3%; Score 920.6; DB 1; Length 1532;  
Best Local Similarity 75.8%; Pred. No. 0;  
Matches 1139; Conservative 0; Mismatches 364; Indels 0;

QY	1	ATGGGTGGCAGAGCGTCA	GTATTAAAGCGGGGAGAA	TTAGATAGATGGGAAAAAATTCGG	60
DB	10	ATGGGTGCTAGGCGCTT	CTGTGCTGTCTGGTGTGAGCTGG	ACAAGTGGGGAAGAATCAGG	69
QY	61	TTAAGGCCAGGGGGAAG	AAAAAATATAGATTAAAA	CATATAGTATGGGCAAGCAGGGAG	120
DB	70	CTAGGCGCTGGTGGCA	GAAGAAGTACAAGCTAA	AGCATTGTGTGGGCTCCAGGGAG	129
QY	121	CTAGAAACGATTCGCA	GTTHAATCCTGGCGCTGT	TAGAAACATCAGAAGCGCTGTAGACAATA	180
DB	130	CTGGAGAGGTTTGCT	GTGAACCTGGCGCTGTGG	AGACCTCTGTGAGGGGTGCAGCGCAGATC	189
QY	181	CTGGGACAGCTACA	ACCATCCCTTCAGACAG	GATCAGAAGACTTAGATCATTTATATAAT	240
DB	190	CTGGGCGAGCTCAG	CGCTCCCTTCGCAACAG	GGCTCTGAGAGCTGAGGTCCTCTGTACAC	249
QY	241	ACAGTAGCAACCTCT	ATTGTGTGCTCAAAGG	ATAGAGTAAAGACACCAAGAGAGCT	300
DB	250	ACAGTGGCTACCT	TGTACTGTGTGCACCA	GAAGATTGATGTGAAGGACACCAAGGAGGCC	309
QY	301	TTAGAGAGATAGAG	AGACGAJAAACAAAG	GTAAAGAAAAGCCACAGCAGCAGCAGCT	360
DB	310	CTGGAGAAGATTG	AGAGAGCAGAACAA	AGTCCAAAGAAGAAGGCCAGCAGGGCTGTGCT	369
QY	361	GACACAGGAAAAC	GAGCAGCGCAGGTCA	GCCAAAATTACCTTATAGTGCAGAACTCTCCAGGGG	420
DB	370	GGCAGAGGCACT	CCAGCCAGGTGTCC	AGACTACCCATTGTGCAGAACTCTCCAGGGC	429
QY	421	CAAAATGGTACAT	CAGGCCATATACCT	CTAGAACCTTTAAATGTCATGGGTAAAGTAGTAGAG	480
DB	430	CAGATGGTGAC	CAGGCCATCTCC	CCCGACCTCGAATGCCCTGGGTGAAAGGTGGTGGAG	489
QY	481	GAGAGGGCTTT	CAGCCCAGAGTA	TAAATACCCATGTTTTTCAGCATTTATCAGAAAGAGGCCACC	540
DB	490	GAGAGGGCTTCT	CCCGCTGAGGTGAT	CCCCCATGTCTCTGCGCCCTGTCTGAGGGGTGCCACC	549
QY	541	CCACAAGATTAA	ACCACTGCTTAA	ACAGTGGGGGGACATCAAGCAGCGCATCTGCAAAATG	600
DB	550	CCCCAGACTG	AAACACCATCTGA	ACAACAGTGGGGGGCCATCAGGCTGCCATGCAAGTG	609
QY	601	TTAAAGAGACCAT	CAATCAGGAGAGCT	GCAGAAATGGGATAGATTGCATTCAGTGTGCATGCA	660
DB	610	CTGAGGAGACCAT	CAATGAGGAGGCT	GTGAGTGGGACAGGGTGCATCTCTGTGCAGGCT	669
QY	661	GGGCTTTGCA	CCAGGCCAGATGAG	AGAACCAAGGGGAGTGCATAGCAGGAACTACT	720
DB	670	GGCCCCATTTG	CCCCCGCCAGATG	AGGGAGCCCAGGGGCTCTGACATTCCTGTGGCACCACC	729
QY	721	AGTACCCTTTCAG	GAAACAAATPAGGAT	GGATGCAAAAATAATCCACTATCCCAAGTAGGAGAA	780
DB	730	TCCACCTCCAG	GAGCAGATTGGCT	GGATGACCAACAAACCCCCCATCTCCCTGTGGGGAA	789
QY	781	ATCTATAAAGAT	TGGATAATCTCTGGG	ATTAAATAGTAAAGATGTATAGCCCTTACC	840
DB	790	ATCTACAAGAG	TGGATCATCTCTGG	GGCTTGAACAAGATTGTGTGAGGATGTACTCTCCCCACC	849
QY	841	AGCATTTCTG	ACATAGACAAGCAG	CAACAAAGAACCTTTTAGAGACTATGTAGACCGGTTTC	900
DB	850	TCCATCTCTG	ACATCAGGCGAGG	CCCCCAGAGCCCTTTCAGGGACTATGTGGAACAGTTTC	909
QY	901	TATAAAACTCT	AAGACCCGACAGC	AGCTTCA CAGGAGGTAAAAATTTGGATGACAGAAACC	960
DB	910	TACAAGACCT	CTGAGGCTGAC	GAGGCTCCCAAGGAGGTGAAGAACTGGAACAGAGACC	969
QY	961	TTGTTGGTCA	AAATGGAACCCAG	ATTGTAAAGACTATTTTAAAGCAATTTGGGACCAAGCA	1020
DB	970	CTGCTGTG	CAGAAATGCAACCT	CTGACTGCAAGACCACTCTGAAAGGCCCTGGGCGCTGCT	1029

QY 1021 GCTACACTAGAAATGATGACAGCATGTGAGGAGTGGGGGACCCGCGCAATAAGCA 1080  
DB 1030 GCACCCCTGAGGAGATGATGACAGCTGCGAGGGTGGGGGCGCCCTGTGTCAAGGCC 1089  
QY 1081 AGAGTTTGGCTGAAGCAATGAGCAAGTAAACAAATTCAGCTACCAATATGATGACAGAGA 1140  
DB 1090 AGGGTGTGCTGAGGCCATGTCCAGGTGACCAACTCCGCCACCATCATGATGACAGAG 1149  
QY 1141 GCGAATTTAGGAACCAAGAAAGACTGTTAAGTGTTCATTTGTGTCGAAGAGGCGAC 1200  
DB 1150 GGCACCTTCAGGAACCAAGAGAGACAGTGAAGTGTTCATTTGTGTCGAAGAGGCGCAC 1209  
QY 1201 ATAGCCAAATTCAGGGGCCCTTAGGAAAGAGGCTGTGGAAATGTGGAAGAGGA 1260  
DB 1210 ATTGCCAGACTGTAGGGCCCCCAGGAGAGAGGCTGTGGAAGTGTGCAAGAGGAGGC 1269  
QY 1261 CACCAATGAAGATTTACTGAGAGACAGGCTAAATTTTAGGGAAGATCTGGCCTTCC 1320  
DB 1270 CACAGATGAAGACTGCAATGAGAGGAGGCGCAACTTCTTGGGCAAAATCTGGCCTCC 1329  
QY 1321 CACAAGGAGGAGGAGGAGATTTTCTCAGAGAGACAGGAGGAGGAGGAGGAGGAGGAG 1380  
DB 1330 CACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1389  
QY 1381 GAGAGCTTCAGGTTTGGGAGAGAGACAACTCCCTCTCAGAGGAGGAGGAGGAGGAGGAG 1440  
DB 1390 GAGTCTTTCAGGTTTGGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1449  
QY 1441 AAGGAAGTGTATCTTTAGCTTCCCTCAGATCACTCTTTGGCAAGACCCCTCGTCACAA 1500  
DB 1450 AAGGAGCTGTACCCCTGGGCTCCCTGAGTCTCTTTGGGAGAGGAGGAGGAGGAGGAG 1509  
QY 1501 TAA 1503  
DB 1510 TAA 1512

RESULT 2  
US-09-017-981-1/c  
Sequence 1, Application US/09017981  
GENERAL INFORMATION:  
APPLICANT: Shiver, John W.  
APPLICANT: Davies, Mary Ellen  
APPLICANT: Freed, Daniel C.  
APPLICANT: Liu, Margaret A.  
APPLICANT: Perry, Helen C.  
TITLE OF INVENTION: Synthetic HIV Gag Genes  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTSEQ For Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/017,981  
FILING DATE: 07-FEB-1997  
APPLICATION NUMBER: GB9705040.5  
FILING DATE: 12-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hand, J. Mark  
REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 19730  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
TELEX:

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-017-981-1

Query Match 1.3%; Score 19.6; DB 1; Length 1532;  
Best Local Similarity 54.1%; Pred. No. 0;  
Matches 40; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
QY 342 GGCACAGCAGCAGCAGCTGACACAGGAAACAGCAGCAGGTCAGCCAAATACCCAT 401  
DB 397 GGGACACCTGGCTGGAGTTGCTGTGCCAGCAGCAGCTGCTGGGCTTCTTCTGACT 338  
QY 402 AGTGCAGAACCTCC 415  
DB 337 TGTCTGTCTCTCC 324

Search completed: January 29, 2007, 11:54:25  
Job time: 0.333333 secs

GenCore version 6.2

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OM nucleic - nucleic search, using sw model

Run on: January 29, 2007, 11:54:23 ; Search time 1 Seconds  
(without alignments)  
13.816 Million cell updates/sec

Title: US-10-780-507-26-COPY  
Perfect score: 1503  
Sequence: 1 atgggtgaggagctcggt.....acgacccatcgcaataa 1503  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1532 residues  
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: US09017981.seq\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
	1	877.4	58.4	1532	1	US-09-017-981-1
	2	18.2	1.2	1532	1	US-09-017-981-1

## ALIGNMENTS

## RESULT 1

US-09-017-981-1  
 ; Sequence 1, Application US/09017981  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shiver, John W.  
 ; APPLICANT: Davies, Mary Ellen  
 ; APPLICANT: Freed, Daniel C.  
 ; APPLICANT: Liu, Margaret A.  
 ; APPLICANT: Petty, Helen C.  
 ; TITLE OF INVENTION: Synthetic HIV Gag Genes  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065-0900  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/017,981  
 ; FILING DATE: 03-FEB-1998  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US60/037,854  
 ; FILING DATE: 07-FEB-1997  
 ; APPLICATION NUMBER: GB9705040.5  
 ; FILING DATE: 12-MAR-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hand, J. Mark  
 ; REGISTRATION NUMBER: 36,545  
 ; REFERENCE/DOCKET NUMBER: 19730  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 732-594-3905  
 ; TELEFAX: 732-594-4720  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1532 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: both  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-09-017-981-1

Query Match 58.4%; Score 877.4; DB 1; Length 1532;  
 Best Local Similarity 74.0%; Pred. No. 0;  
 Matches 1112; Conservative 0; Mismatches 391; Indels 0; Gaps 0;  
 QY 1 ATGGGTGCGGAGCGTGGTATTAAAGCGGGGAAATTAGATAGTGGGAAATAATTCGG 60  
 DB 10 ATGGGTGCTAGGCGTCTGTGCTGTCTGGTGGTGGAGCTGGACAAAGTGGGAGAGATCAGG 69  
 QY 61 TTAAGCCGAGGGGAAAGAAAATAATAAATTAACATATAGTATGGGCAAGCAGGAG 120  
 DB 70 CTGAGGCGCTGGTGGCAGAGAGAGTACAGCTAAAGCACAATTGTGGGCTCCAGGAG 129  
 QY 121 CTAGAACGATTTCAGTCAATCTCGGCTCTGTAGAAAATCAGAAAGCTCAGACGAATA 180  
 DB 130 CTGAGAGGTTTGTGTGAACCTTGGCTCTGTGGAGACCTCTGAGGGGTTCAGGCAGATC 189  
 QY 181 CTGGAACAGCTACATCCATCCCTTCAGACAGGATCAGAAAGACTTAATCATTTATATAT 240

DB 190 CTGGGCCAGCTCCAGCCCTCCCTGCAACAGAGCTCTGAGGAGCTGAGGTCCCTGTACAAC 249  
 QY 241 ACGGTAGCAACCTCTATTGTGTGATCAAAATATAGAGGTAAAGACACCAAGGATGCT 300  
 DB 250 ACAGTGGCTACCTCTGTGTGATCCAGAGATTGATGTGAAGGACCAAGGAGGCC 309  
 QY 301 TTAGAAAAATAGAGGAGAACAAACAAAATTTAGAAAAGGGCAGCAGCAGCAGCAGCT 360  
 DB 310 CTGGGAAAGATTGAGGAGAGCAGAAACAGTCCAAGAAAGAGGCCCGCAGCGGTCTGCT 369  
 QY 361 GACACAGGAAACAGCAACCCCGGTAGCCAAATATACCTTATAGTGCAGATATAGCAGGGG 420  
 DB 370 GGCACAGGCNACTCCAGCCAGGTGTCACAGACTACCCCATTTGTCAGAACCTCCAGGGC 429  
 QY 421 CAAATGGTACATCAGGCCATATCACTAGAACTTTAAATGCAATGGGTAAAGTAGTAGAA 480  
 DB 430 CAGATGGTGCACAGGCCATCTCCCCCGGACCTGAATGCCCTGGGTGAAGGTGGTGAG 489  
 QY 481 GAGAGGGCTTTACAGCCCGAGTATACCCATGTTTTCAGCATTTATCAGAAAGGAGCCACC 540  
 DB 490 GAGAAAGGCTTCTCCCTGAGGTGATCCCATGTTCTCTGCCCTGTCTGAGGGTGGCCACC 549  
 QY 541 CCACAAGATTTAAACACCATGCTAAACACAGTGGGGGACATCAACAGCAGCCATGCAAAATG 600  
 DB 550 CCCAGGACCTGAACACCATGCTGAACACAGTGGGGGCCATCAGGCTGCCATGCAGATG 609  
 QY 601 TTAAAGAAACCATCAATGAGGAAAGCTGAGAAATGGGATAGATTGCACCCAGTGCATGCA 660  
 DB 610 CTGAAGGAGACCATCAATGAGGAGCTGCTGAGTGGGACAGAGCTGCTGTCGACGCT 669  
 QY 661 GGGCTTATGCACAGCCAGATGAGAAACCAAGGGGAGTGCATACAGCAAGAACTACT 720  
 DB 670 GGGCCCATTTGCCCGCCAGATGAGGGAGCCAGGGCTCTGACATTTGCTGGCAGCCACC 729  
 QY 721 AGTAGCCCTTCAGGAAACAAATAGGATGGATGACACATAATCCACCTATCCAGTAGGAGA 780  
 DB 730 TCCACCTCCAGGAGCAGATTGGCTGGATGACCAACACCCCCCATCTCTGTGGGGAA 789  
 QY 781 ATCTATAAAGATGGATTAATCATGGATTAATAAATAGTAAGATGTATAGCCCTTACC 840  
 DB 790 ATCTACAAGAGGTGGATCATCTCGGCTGTAACAAGATTGTGAGGATGTACTCCCCCACC 849  
 QY 841 AGCATTTCTGACATTAAGACNAGGACCAAGGAGACCTTTAGAGATTATGTTGACCCGTT 900  
 DB 850 TCCATCTCGACATCAGGAGGCGCCCAAGAGGACCTTCAGGACTATGTGGACAGGTTC 909  
 QY 901 TATAAACTCTAAGAGCCGAGCAAGCTTCAAGGAGGTAAATAATTTGGATGACAGAAACC 960  
 DB 910 TACAAGACCTTGAGGCTGAGCAGGCTCCAGGAGGTGAGNACTGGATGACAGAGACC 969  
 QY 961 TTGTTGGTCCAAAATTCGAAACCCAGATTGTAAAGCCATTTTAAAGCATTTAGACCCAGCA 1020  
 DB 970 CTGCTGGTGCAGATGCCAACCTCTGACTCAAGAGCCATCTCTGAAGGCCCTGGGCCCTGT 1029  
 QY 1021 GCTACACTAGAAATATGATGACAGCATGTGAGGAGTGGGAGGCGCCAGCCATTAAGCA 1080  
 DB 1030 GGCACCTTGAGGAGATGATGACAGCTCCAGGGGGTGGGGGGCCCTGCTGTCACAGGCC 1089  
 QY 1081 AGAGTTTTTGGCAGAGCAATGAGCCAGCAAGCAAAATTCAGTACCAATATGATGACAGG 1140  
 DB 1090 AGGTGCTGGCTGAGGCCATGTCCCAAGGTGACCACTCCGCCACCATCATGATGACAGG 1149  
 QY 1141 GGCATTTTAAAGGGCCAAAGAAAGTGTAAATGTTTCAATTTGTGGCAAGAGGGGCAC 1200  
 DB 1150 GGCNACTTCAGGAAACAGAGGAGAGCAGTGAAGTGTCTCAACTGTGGCAAGGTGGGCCAC 1209  
 QY 1201 ATAGCAGAAATTCAGGGCCCTTAGAAAAAAGGGCTGTGGAAATGTGGAAGAGGAGGA 1260  
 DB 1210 ATTGCCAAGAACTGTAGGGCCCTCCAGAAAGAGGGCTGTGGAGTGTGCAAGGAGGGC 1269  
 QY 1261 CACCAATCAAGATTTGATCTAGACAGCAGGCTTAATTTTTTAGGGAAGATCTGGCCCTTC 1320

Db 1270 CACCAGATGAAGGACTGCAATGAGAGGCGCAACTTCTGGGCAAAATCTGGCCCTCC 1329  
 Qy 1321 CACAAGGGAGGCCAGGGAATTTCTCCAAAGCAGGCGCAGCAACAGCCCCCACCAGAA 1380  
 Db 1330 CACAAGGGAGGCCCTGGCAACTTCTCCAGTCAGGCGCTGAGGCCACAGCCCCCTCCCGAG 1389  
 Qy 1381 GAGAGCTTCAAGTTTGGGGAGGAGACAACTCCCTCCAGAGCAGGAGCGAGGAC 1440  
 Db 1390 GAGTCTTCAAGTTTGGGGAGGAGAGACACCCCGAGCGAGAGGAGGCCATGAC 1449  
 Qy 1441 AAGGAACAGTATCCCTTGACTTCCCTCAGATCACTTTTGGCAACGACCCCATCGTCACAA 1500  
 Db 1450 AAGGAGCTGTACCCCTGGGCTCCCTGAGGTCCCTGTTGGCAACGAGACCCCTCTCCAG 1509  
 Qy 1501 TAA 1503  
 Db 1510 TAA 1512

RESULT 2

US-09-017-981-1/C  
 ; Sequence 1, Application US/09017981  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shiver, John W.  
 ; APPLICANT: Davies, Mary Ellen  
 ; APPLICANT: Freed, Daniel C.  
 ; APPLICANT: Liu, Margaret A.  
 ; APPLICANT: Perry, Helen C.  
 ; TITLE OF INVENTION: Synthetic HIV Gag Genes  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065-0900  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FastSeq for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/017,981  
 ; FILING DATE: 03-FEB-1998  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US60/037,854  
 ; FILING DATE: 07-FEB-1997  
 ; APPLICATION NUMBER: GB9705040.5  
 ; FILING DATE: 12-MAR-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hand, J. Mark  
 ; REGISTRATION NUMBER: 36,545  
 ; REFERENCE/DOCKET NUMBER: 19730  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 732-594-3905  
 ; TELEFAX: 732-594-4720  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1532 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: both  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-09-017-981-1

Query Match: 1.2%; Score 18.2; DB 1; Length 1532;  
 Best Local Similarity 61.7%; Pred. No. 0;  
 Matches 29; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1293 TAAATTTTATAGGAAAGATCTGGCTTCCCAAGGGAAGGCCAGGGA 1339  
 Db 1517 TTATTTTACTGGGAGGAGGGGTCTGTTCCTCCAAACAGGGACCTCAGGGA 1471

Search completed: January 29, 2007, 11:54:25  
 Job time : 0.333333 secs

Date: Mon Jan 29 12:32:01 2007

About: Results were produced by the GenCore software, version 6.2,

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**Command line parameters:**

```

-THR1 -MODEL=frames+ r2d_model -DEV=soft -Qnew_seq -DB=new pep2 -SUPPLY=pfis
-OUT=507aa.res -MINMAX=0.1 -LOOPL=0 -LOOPEXT=0 -UNITS=big -START=1 -END=1
-MATRIX=blomsum2 -TRANS=human40.cdi -LIST=45 -DOCAI=200 -THR SCORES=pct
-THR MAX=100 -THR MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pfis -NORM=ext
-HEADSIZE=0 -MINLEN=0 -MAXLEN=20000000 -NCPU=6 -NO_XLPFY -NEG SCORES=0
-LONGLOO -MINDIST=10 -XGAPOP=1.0 -XGAPEXT=0.5 -XGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```

**Search information:**

Query: US-10-780-507-25-COPY

Query: 03-10-780-307-23-COF1  
Query length: 1503

Query result: 1503  
Database: new\_nen2:\*

Database: new.pep2: Database sequences: 6

Database sequence: 6  
Database length: 3058Database length: 3058  
Search time (sec): 5

search time (sec): 5

**Score list:**

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation	..
new.pep2:US-09-017-981-1-1-FRAME1	-	2602.00	241.39	1.2e-10	510	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME2	-	2015.00	195.14	4.6e-08	510	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME3	-	917.00	108.61	0.0031	509	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME4	-	896.00	106.96	0.0038	509	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME5	-	880.00	106.94	0.0035	510	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME6	-	507.00	76.31	0.1904	510	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME7	-	58.50	40.96	8.32	510	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME8	-	48.50	40.18	8.61	510	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME9	-	45.50	39.94	8.71	509	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME10	-	42.50	39.70	8.79	509	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME11	-	42.50	39.70	8.77	510	Entered	[bobryen 29-01-98]
new.pep2:US-09-017-981-1-1-FRAME12	-	40.50	39.55	8.82	510	Entered	[bobryen 29-01-98]

Sequence name: new.pep2:US-09-017-981-1-FRAME1

**Sequence documentation:**

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sequence documentation:
: Entered [bob] 29-Jan-07 11:58]
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US-09-017-981-1-FRAMB1

Alignment of: US-10-780-507-25-COPY X US-09-017-981-1-FRAME1

[illegible]

24

Quality:	2602.00	Score:	1.23e-10
Matching length:	500	Total length:	500
Matching Percent Similarity:	99.40	Matching Percent Identity:	98.40
Total Similarity:	99.40	Total Percent Identity:	98.40

**Alignment:**

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4 MetGlyAlaArgAlaSerValLeuSerGlyGlyGluLeuAspLysTrpG1 20

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11 TAGTATGGGCAAGCAGGGAGCTAGAACGATTCCGAGTTAATCCTGGCCTG 150

77 leValTrpAlaSerArgGluLeuGluuArgPheAlaValAsnProGlyLeu 53

11 TTAGAAACATCAGAAGCTGTAGACAAATACTGGGACAGCTACAACCATC 200

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1103 MetTrpProThrLeuProGlnLeuLeuLysHisPheThrValPheLeuTrpPh 124
1104 MetTrpProThrLeuProGlnLeuLeuLysHisPheThrValPheLeuTrpPh 124
1105 CTTAAATATGCTCTCTGCTGATCATATTATGCTGCTGCTGCTGCTGCTGCT 1103
1106 eLeuLysLeuProLeuLeuLysHisPheThrValPheLeuTrpPh 141
1107 TCATTGCTTTCAGCAAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1053
1108 spMetAlaSerAlaSerThrLeuAlaLeuProGlyProProThrProTrp 157
1109 TGACATGCTCTCATCAATTTCTTCTAGTGTAGTGTGCTGCTGCTGCTGCTGCT 1003
1110 GlnAlaValIleIleSerSerArgValAlaAlaGlyProArgAlaPheAr 174
1111 TAAATAGTCTTACAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
1112 gMetValLeuGlnSerGlyLeuAlaPheCysThrSerArgValSerValI 191
1113 TCATCCAAATTTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
1114 leGlnPhePheThrSerTrpGluAlaCysSerAlaLeuArgValLeuAsn 207
1115 TAGAACCGGTCTACATAGTCTCTTAAAGGCTTCTTGGTCTGCTGCTGCTGCT 853
1116 LeuSerThrSerLeuLysGlySerLeuGlyProCysLeuMetSerArgMe 224
1117 GTCCAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803
1118 tGluValGlyGluTrpIleLeuThrIleLeuPheArgProArgMetIleH 241
1119 GGATTATCCATCTTTATAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
1120 lsLeuLeuIleSerProThrGlyMetGlyLeuLeuValIleGlnPro 257
1121 GTCCATCCATCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 703
1122 IleCysSerTrpArgValGluValAlaProAlaMetSerGluProLeuGl 274
1123 ACTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
1124 YserLeuIleTrpProGlyAlaMetGlyProAlaCysThrGlyCysSerL 291
1125 CTGATGCAATCTATCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
1126 euSerHisSerAlaAlaSerSerLeuMetValSerPheSerIleCysMet 307
1127 AACATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
1128 AlaAlaTrpProProThrValPheSerMetValPheArgSerTrpGlyVa 324
1129 TAAATCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 503
1130 lAlaProSerAspArgAlaGluAsnMetGlyIleThrSerGlyGluLysA 341
1131 CTTCTGGGCTGAAAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 453
1132 lAlaPheSerSerThrThrPheThrGlnAlaPheArgValArgGlyGluMet 357
1133 GTTCTAGGTGATATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403
1134 AlaTrpCysThrIleTrpProTrpArgPheCysThrMetGlyPheTrpAs 374
1135 TATAGGTAATTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 353
1136 pThrTrpLeuGluLeuProValProAlaAlaCysTrpAlaPhePheL 391
1137 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
1138 euAspLeuPheCysSerSerIlePheSerArgAlaSerLeuValSer 407
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Sequence name: new.pdp2.US-09-017-981-1-FRAME4

Sequence documentation:

; Entered [bobryen 29-Jan-07 12:02]

US-09-017-981-1-FRAME4

Alignment of: US-10-780-507-25-COPY x US-09-017-981-1-FRAME4

Alignment segment 1/1: (-)

Quality:	2015.00	Score:	4.62e-08
Matching length:	500	Total length:	500
Matching Percent Similarity:	90.60	Matching Percent Identity:	79.60
Total Percent Similarity:	90.60	Total Percent Identity:	79.60
Gaps:	0	Stops:	13

Alignment:

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1502 TATTGTGACGAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1453
8 TyrTrpGluGluGlySerLeuProAsnArgAspLeuArgGluAlaArgL 24
1452 ATACAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1403
24 YTrpSerSerLeuSerMetGlySerCysPheTrpLeuGlyValValPheS 41
1402 CTTCCCAACCTGAAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1353
41 erSerProAsnLeuLysAspSerSerGlyGlyAlaValGlySerGlyLeu 57
1352 CTCTGAAGAAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
58 AspTrpArgLysLeuProGlyLeuProLeuTrpGluGlyGlnIleLeuPr 74
1302 TAAAAAATAGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253
74 oArgLysLeuAlaCysLeuSerLeuGlnSerPheIleTrpProSerL 91
1252 TTCCCAATTCACAGCCCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1203
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